

For the Record

A Population-Genetic Study of the DYS385 Haplotypes in Two Spanish Populations and the African Immigrant Population in Spain

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Keywords: forensic science, short tandem repeat, Y chromosome, polymorphism, haplotype, population genetics, DYS385, forensic analysis

Whole EDTA blood was obtained by venipuncture from 137 unrelated individuals from the south-west of Spain (Cádiz, Huelva and Sevilla), 100 unrelated individuals from the autochthonous population of the Canary Islands, 119 unrelated immigrants from the black population of West Africa and also 30 unrelated immigrants from the north of Morocco. For the autochthonous Canary Islands group only those individuals who descend from at least three generations born in the Canary Islands qualified for selection. The DNA was extracted using Chelex 100 protocol as described by Walsh et al. (1).

Aliquots of 5 µL the extracts with a DNA content of approximately 5 ng/µL were used for amplification. PCR primers used were described by S. Gerken et al. (Salt Lake City, USA, unpublished) and were synthesized as deposited in Genome Database

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(GDB accession numbers L36701 and L36702) (2,3). The amplification conditions complied with the methodology described by Schneider et al. (2,3) in a Perkin Elmer 9600 thermocycler.

Electrophoresis was carried out on 4% polyacrylamide denaturing sequencing gels on a 377 automated system (Applied Biosystems Division/Perkin Elmer). Genotype classification was made using Genescan PCR analysis software with the Local Southern method and by side-to-side comparison with allelic ladders kindly provided by Dr. P. M. Schneider (Institut für Rechtsmedizin, Mainz). Haplotype diversity was calculated according to Nei (4).

The complete data are available to any interested researcher upon request.

References

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TABLE 1—DYS385 genotype frequencies.

Allele Combination	African Black Immigt. n = 119	Morocco Immigt. n = 30	Canary Islands (Spain) n = 100	South West Spain n = 137	Allele Combination	African Black Immigt. n = 119	Morocco Immigt. n = 30	Canary Islands (Spain) n = 100	South West Spain n = 137
10-13			0.0100	0.0145	14-15	0.0361	0.0333	0.0100	0.0145
10-14			0.0300	0.0291	14-16	0.0672		0.0200	0.0072
11-11			0.0100	0.0072	14-17	0.0080		0.0400	0.0072
11-12			0.0500	0.0145	14-18	0.0168		0.0100	0.0072
11-13		0.0333	0.0500	0.0218	15-15	0.0361		0.0300	0.0218
11-14			0.3400	0.3868	15-16	0.1513			0.0072
11-15		0.0333	0.0700	0.1021	15-17	0.0672			0.0072
11-16				0.0072	15-18	0.0168			0.0072
12-12			0.0100	0.0072	15-20	0.0080			
12-13				0.0218	16-16	0.1428	0.0666		0.0218
12-14			0.0100	0.0291	16-17	0.0924		0.0200	0.0145
12-15	0.0080		0.0300	0.0072	16-18	0.0672			0.0145
12-16				0.0145	16-19	0.0080		0.0100	
12-17			0.0100	0.0072	16-20	0.0080			0.0072
12-18				0.0072	17-17	0.0672			0.0072
13-13			0.0500		17-18	0.0420			0.0218
13-14		0.6000	0.0300	0.0510	17-19	0.0361			
13-15	0.0250	0.1333	0.0700	0.0291	18-18	0.0250			
13-16	0.0250		0.0300	0.0291	18-21	0.0080			
13-17				0.0072	19-19	0.0080			
13-18			0.0200		19-20				0.0072
13-19			0.0200	0.0072	19-21				0.0072
14-14	0.0361	0.0666	0.0200	0.0145					
HDV	0.9200	0.6100	0.8580	0.8290					

HDV: Haplotype diversity value.